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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
TIME: 10:17:37

Input Set: I147346.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: YISSUM Research Development Company of the Hebrew
2 YARKONI, Shai
3 NECHUSHTAN, Amotz
4 LORBERBOUM-GALSKI, Haya
5 MARIANOVSKI, Irina
6 <120> TITLE OF INVENTION: CHIMERIC TOXINS FOR TARGETED THERAPY
7 <130> FILE REFERENCE: 1268-073
8 <140> CURRENT APPLICATION NUMBER: US/09/147,346
9 <141> CURRENT FILING DATE: 1999-03-01
10 <150> EARLIER APPLICATION NUMBER: PCT\IL97\00180
11 <151> EARLIER FILING DATE: 1996-06-04
12 <160> NUMBER OF SEQ ID NOS: 4
13 <170> SOFTWARE: PatentIn Ver. 2.1
14 <210> SEQ ID NO 1
15 <211> LENGTH: 1152
16 <212> TYPE: DNA
17 <213> ORGANISM: Escherichia coli
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26 acctgcccgg tcgcccggcg tgaatgcgcg ggcccggcgg acagcggcga cgccctgctg 480
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30 gtcttcggcg gggtgcgcg gcgcagccag gacctcgacg cgatctggcg cggtttctat 720
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32 ggccggatcc gcaacgggtg cctgctgcgg gtctatgtgc cgcgctcgag cctgccgggc 840
33 ttctaccgca ccagcctgac cctggccggc ccggaggcgg cgggcgaggt cgaacggctg 900
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36 atccccaccg acccgcgcaa cgtcggcggc gacctcgacc cgtccagcat ccccgacaag 1080
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42 <213> ORGANISM: Escherichia coli
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45      1      5      10      15
46    Ala His Met Ala Glu Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His
47      20      25      30
48    Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro
49      35      40      45
50    Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
51      50      55      60
52    Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
53      65      70      75      80
54    Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly
55      85      90      95
56    Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
57      100      105      110
58    Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp
59      115      120      125
60    Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val
61      130      135      140
62    Ala Ala Gly Ala Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu
63      145      150      155      160
64    Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp
65      165      170      175
66    Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
67      180      185      190
68    Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly
69      195      200      205
70    Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly
71      210      215      220
72    Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr
73      225      230      235      240
74    Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
75      245      250      255
76    Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
77      260      265      270
78    Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu
79      275      280      285
80    Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
81      290      295      300
82    Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly
83      305      310      315      320
84    Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
85      325      330      335
86    Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
87      340      345      350
88    Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro
89      355      360      365
90    Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
91      370      375      380

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92 <210> SEQ ID NO 3
93 <211> LENGTH: 1869
94 <212> TYPE: DNA

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99   ccggccatcg ccgacaccaa cggccagggc gtgctgctact actccatggt cctggagggc 180
100  ggcaacgacg cgtcgcagct ggccatcgac aacgccctca gcatcaccag cgacggcctg 240
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104  atctacacca tcgagatggg cgacgagttg ctggcgaagc tggcgcgcg tggcaccttc 480
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106  gtcagcgtgg tcatggccca gaccagccg cgccgggaaa agcgtgtag cgaatggggc 600
107  agcggcaagg tggtgtgctt gctcgaccgg ctggcagggg tctacaacta cctcgcccg 660
108  caacgctgca acctcgacga tacctgggaa ggcaagatct accgggtgct cgccggcaac 720
109  ccggcggaag atgacctgga catcaaacc acggtcatca gtgaagagct ggagtttccc 780
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126  cccaccgacc cgcgcaacgt cggcgcgac ctcgaccgt ccagatccc cgacaaggaa 1800
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137             20             25             30
138   Arg Ser Ser Arg Met Ser Val Asp Pro Ala Ile Ala Asp Thr Asn Gly
139             35             40             45
140   Gln Gly Val Leu His Tyr Ser Met Val Leu Glu Gly Gly Asn Asp Ala
141             50             55             60
142   Leu Glu Leu Ala Ile Asp Asn Ala Leu Ser Ile Thr Ser Asp Gly Leu
143             65             70             75             80
144   Thr Ile Arg Leu Glu Gly Gly Val Glu Pro Asn Lys Pro Leu Arg Tyr

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146	Ser	Tyr	Thr	Arg	Gln	Ala	Arg	Gly	Arg	Trp	Ser	Leu	Asn	Trp	Leu	Val
147					100					105				110		
148	Pro	Ile	Gly	His	Glu	Lys	Pro	Ser	Asn	Ile	Lys	Val	Phe	Ile	His	Glu
149			115						120					125		
150	Leu	Asn	Ala	Gly	Asn	Gln	Leu	Ser	His	Met	Ser	Pro	Ile	Tyr	Thr	Ile
151		130						135					140			
152	Glu	Met	Gly	Asp	Glu	Leu	Leu	Ala	Lys	Leu	Ala	Arg	Asp	Ala	Thr	Phe
153		145				150					155				160	
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156	Ser	His	Ala	Gly	Val	Ser	Val	Val	Met	Ala	Gln	Thr	Gln	Pro	Arg	Arg
157			180						185					190		
158	Glu	Lys	Arg	Trp	Ser	Glu	Trp	Ala	Ser	Gly	Lys	Val	Leu	Cys	Leu	Leu
159			195					200					205			
160	Asp	Pro	Leu	Asp	Gly	Val	Tyr	Asn	Tyr	Leu	Ala	Gln	Gln	Arg	Cys	Asn
161		210						215				220				
162	Leu	Asp	Asp	Thr	Trp	Glu	Gly	Lys	Ile	Tyr	Arg	Val	Leu	Ala	Gly	Asn
163		225				230					235				240	
164	Pro	Ala	Lys	His	Asp	Leu	Asp	Ile	Lys	Pro	Thr	Val	Ile	Ser	Glu	Glu
165					245					250					255	
166	Leu	Glu	Phe	Pro	Glu	Gly	Gly	Ser	Leu	Ala	Ala	Leu	Thr	Ala	His	Gln
167			260						265					270		
168	Ala	Cys	His	Leu	Pro	Leu	Glu	Thr	Phe	Thr	Arg	His	Arg	Gln	Pro	Arg
169			275						280				285			
170	Gly	Trp	Glu	Gln	Leu	Glu	Gln	Cys	Gly	Tyr	Pro	Val	Gln	Arg	Leu	Val
171		290					295					300				
172	Ala	Leu	Tyr	Leu	Ala	Ala	Arg	Leu	Ser	Trp	Asn	Gln	Val	Asp	Gln	Val
173		305				310					315				320	
174	Ile	Arg	Asn	Ala	Leu	Ala	Ser	Pro	Gly	Ser	Gly	Gly	Asp	Leu	Gly	Glu
175					325					330					335	
176	Ala	Ile	Arg	Glu	Gln	Pro	Glu	Gln	Ala	Arg	Leu	Ala	Leu	Thr	Leu	Ala
177			340						345					350		
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179			355						360				365			
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181		370					375					380				
182	Ala	Gly	Glu	Cys	Ala	Gly	Pro	Ala	Asp	Ser	Gly	Asp	Ala	Leu	Leu	Glu
183		385				390					395				400	
184	Ala	Asn	Tyr	Pro	Thr	Gly	Ala	Glu	Phe	Leu	Gly	Asp	Gly	Gly	Asp	Val
185					405					410					415	
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187				420					425					430		
188	Gln	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	Gly	Tyr	Val	Phe	Val	Gly	Tyr
189			435						440				445			
190	His	Gly	Thr	Phe	Leu	Glu	Ala	Ala	Gln	Ser	Ile	Val	Phe	Gly	Gly	Val
191		450					455					460				
192	Arg	Ala	Arg	Ser	Gln	Asp	Leu	Asp	Ala	Ile	Trp	Arg	Gly	Phe	Tyr	Ile
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201				530		535
202	Pro	Leu	Arg	Leu	Asp	Ala
203				545		550
204	Leu	Glu	Thr	Ile	Leu	Gly
205				565		570
206	Pro	Ser	Ala	Ile	Pro	Thr
207				580		585
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VERIFICATION SUMMARY
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